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Timestamp: Fri Aug 31 08:56:29 EDT 2007

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Application No: 10522106 Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-21 07:56:35.977
Finished: 2007-08-21 07:56:38.925
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 948 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 24
Actual SeqID Count: 24

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
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SEQUENCE LISTING

<110> Kogel, Karl-Heinz
Huckelhoven, Ralph
Trujillo, Marco

<120> Method for Obtaining the pathogenic resistance in plants

<130> 12810-00067-US

<140> 10522106

<141> 2007-08-21

<160> 24

<170> PatentIn version 3.3

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<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (2)..(337)

<223> coding for NADPH oxidase (fragment)

<400> 1

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Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
    20          25          30
cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat 145
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn
    35          40          45
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Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
    50          55          60
cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat 241
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
    65          70          75          80
gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa 289
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
    85          90          95
cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc 337
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<213> Hordeum vulgare

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<222> (55)..(55)

<223> The 'Xaa' at location 55 stands for Gly.

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Pro	Asn	Phe	Lys	Arg	Val	Leu	Ser	Lys	Val	Ala	Ala	Lys	His	Pro	Tyr	
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Ala	Lys	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ala	Pro	Val	Leu	Ala	Gln	Glu	
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<222> (1)..(2829)

<223> coding for NADPH oxidase

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acg	aca	ccg	cgg	tcg	ctg	agc	acg	ggc	tcg	tcg	ccg	cgc	ggg	tcc	gac	96
Thr	Thr	Pro	Arg	Ser	Leu	Ser	Thr	Gly	Ser	Ser	Pro	Arg	Gly	Ser	Asp	
			20					25					30			
gac	cgg	agc	tcc	gac	gac	ggg	gag	gag	ctg	gtc	gag	gtc	acg	ctc	gac	144
Asp	Arg	Ser	Ser	Asp	Asp	Gly	Glu	Glu	Leu	Val	Glu	Val	Thr	Leu	Asp	
		35				40						45				
ctg	cag	gac	gac	gac	acc	att	gtg	ctt	cgg	agc	gtc	gag	ccc	gcg	gcg	192
Leu	Gln	Asp	Asp	Asp	Thr	Ile	Val	Leu	Arg	Ser	Val	Glu	Pro	Ala	Ala	
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gcg	gcg	gcg	gcg	ggg	gtg	ggg	gcg	ggg	gcg	ggg	gcg	gcg	tcg	gcg	cgg	240
Ala	Ala	Ala	Ala	Gly	Val	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Ser	Ala	Arg	
	65				70				75					80		
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Gly	Glu	Leu	Thr	Gly	Gly	Pro	Ser	Ser	Ser	Ser	Ser	Arg	Ser	Arg	Ser	
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Pro	Ser	Ile	Arg	Arg	Ser	Ser	Ser	His	Arg	Leu	Leu	Gln	Phe	Ser	Gln	
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Glu	Leu	Lys	Ala	Glu	Ala	Met	Ala	Arg	Ala	Arg	Gln	Phe	Ser	Gln	Asp	
		115				120						125				
ctg	acc	aag	cgg	ttc	ggc	cgc	agc	cac	agc	cgc	agc	gaa	gcg	cag	gcg	432
Leu	Thr	Lys	Arg	Phe	Gly	Arg	Ser	His	Ser	Arg	Ser	Glu	Ala	Gln	Ala	
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Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Ala Arg Arg Gln	
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cgc gcg cag ctc gac cgc aca cgc tcc ggc gcc cac aag gcg ctc cgc	528
Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg	
165 170 175	
ggc ctc cgc ttc atc agc agc aac aag gcc aac aac gcc tgg atg gag	576
Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu	
180 185 190	
gtg cag gcc aac ttc gac cgc ctc gcc cgc gac ggc tac ctc tcc cgc	624
Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg	
195 200 205	
tcc gac ttc gcc gaa tgc atc ggg atg acg gaa tcg aag gag ttc gcg	672
Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala	
210 215 220	
ctc gag ctg ttc gac acg ctg agc cgg cga cga cag atg aag gtg gac	720
Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Arg Gln Met Lys Val Asp	
225 230 235 240	
acg att aac aag gat gaa ctc cgc gag atc tgg cag cag atc acc gat	768
Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp	
245 250 255	
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Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys	
260 265 270	
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Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met	
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Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu	
290 295 300	
gag tac gcc gct ttg atc atg gag gag ctt gat cct gaa ggg ctc gcc	960
Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Gly Leu Gly	
305 310 315 320	
tac att gag cta tgg caa ttg gag aca ctt ctg ttg cag aaa gat acc	1008
Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr	
325 330 335	
tat atg aac tat agt cag gcc ctt agt tac aca agc caa gca ctg agc	1056
Tyr Met Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser	
340 345 350	
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Gln Asn Leu Ala Gly Leu Arg Lys Lys Ser Ser Ile Arg Lys Ile Ser	
355 360 365	
acc tct tta agc tac tat ttc gag gac aac tgg aaa cgt tta tgg gtg	1152
Thr Ser Leu Ser Tyr Tyr Phe Glu Asp Asn Trp Lys Arg Leu Trp Val	
370 375 380	
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Leu Ala Leu Trp Ile Gly Ile Met Ala Gly Leu Phe Thr Trp Lys Phe	
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Thr Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu Asn Met Ala Ile	
420 425 430	
atc ctc ctg cca gta tgc cgt aac acc att act tgg ttg cga agt aca	1344
Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Ser Thr	
435 440 445	

agg gct gca cgg gca cta cct ttt gat gac aac atc aac ttc cac aag	1392
Arg Ala Ala Arg Ala Leu Pro Phe Asp Asp Asn Ile Asn Phe His Lys	
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act att gca gca gca att gtg gtt ggt ata atc ctc cat gca ggg aac	1440
Thr Ile Ala Ala Ala Ile Val Val Gly Ile Ile Leu His Ala Gly Asn	
465 470 475 480	
cac ctt gta tgc gat ttt cca cgg tta ata aaa tca tca gat gag aag	1488
His Leu Val Cys Asp Phe Pro Arg Leu Ile Lys Ser Ser Asp Glu Lys	
485 490 495	
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Tyr Ala Pro Leu Gly Gln Tyr Phe Gly Glu Ile Lys Pro Thr Tyr Phe	
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Thr Leu Val Lys Gly Val Glu Gly Ile Thr Gly Val Ile Met Val Val	
515 520 525	
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Cys Met Ile Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser	
530 535 540	
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Leu Val Lys Leu Pro Arg Pro Phe Asp Lys Leu Thr Gly Phe Asn Ala	
545 550 555 560	
ttt tgg tat tct cat cat ctg ttc atc att gtg tat atc gcg ctc att	1728
Phe Trp Tyr Ser His His Leu Phe Ile Ile Val Tyr Ile Ala Leu Ile	
565 570 575	
gtt cat gga gag tgt cta tac ctt att cat gtc tgg tac aga aga acg	1776
Val His Gly Glu Cys Leu Tyr Leu Ile His Val Trp Tyr Arg Arg Thr	
580 585 590	
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595 600 605	
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Ile Leu Arg Phe Phe Arg Ser Gly Ser Tyr Ser Val Arg Leu Leu Lys	
610 615 620	
gtg gcc ata tat cca ggt aat gtt ttg aca ctg caa atg tcc aag cct	1920
Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro	
625 630 635 640	
ccc acg ttc cgt tac aag agt gga caa tat atg ttt gtt caa tgt cca	1968
Pro Thr Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro	
645 650 655	
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Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro	
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Gly Asp Asp Tyr Leu Ser Ile His Val Arg Gln Leu Gly Asp Trp Thr	
675 680 685	
cga gaa ctc aag aga gta ttt gct gca gct tgt gag ccc cca gcg ggt	2112
Arg Glu Leu Lys Arg Val Phe Ala Ala Ala Cys Glu Pro Pro Ala Gly	
690 695 700	
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Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Thr Thr Lys Lys Ile Leu	
705 710 715 720	
ccc aag ctt ctg att gat gga ccg tat ggt tct cct gct cag gat tac	2208
Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ser Pro Ala Gln Asp Tyr	
725 730 735	
agc aag tat gat gtt tta tta ctt gtt gga tta gga att ggt gcg aca	2256
Ser Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr	
740 745 750	

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Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Ile Lys Met	
755 760 765	
gag gaa gag gag gat gct tct act gat ctt tat cca cca atg ggt cgg	2352
Glu Glu Glu Glu Asp Ala Ser Thr Asp Leu Tyr Pro Pro Met Gly Arg	
770 775 780	
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Asn Lys Pro His Val Asp Leu Gly Thr Leu Met Thr Ile Thr Ser Arg	
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Pro Lys Lys Ile Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr	
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cgt gag caa ggc tct ttt gat tgg ttc aaa gga gtc atg aat gaa att	2496
Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Ile	
820 825 830	
gct gac ttg gat caa agg aat atc att gag atg cac aac tac cta aca	2544
Ala Asp Leu Asp Gln Arg Asn Ile Ile Glu Met His Asn Tyr Leu Thr	
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agc gtc tat gag gag ggg gat gcc agg tca gca ctc atc acc atg ctc	2592
Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu	
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Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr	
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Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser	
885 890 895	
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aac ggg aaa tgc aca acg aag ttc gaa ttc cat aag gag cat ttc tga	2832
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<212> PRT

<213> Oryza sativa

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Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala	
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Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln	
100 105 110	

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